

# CTD profiles collected with RV Connecticut on the Continental shelf and slope south of Montauk, NY on 14-15 June 2022.

**Website:** <https://www.bco-dmo.org/dataset/879380>

**Data Type:** Cruise Results

**Version:** 1

**Version Date:** 2022-09-16

## Project

» [Collaborative Research: Combining single-cell and community omics to test hypotheses about diversity and function of planktonic ciliates](#) (Ciliate Omics)

Contributors	Affiliation	Role
<a href="#">McManus, George</a>	University of Connecticut (UConn)	Principal Investigator, Contact
<a href="#">Katz, Laura A.</a>	Smith College	Co-Principal Investigator
<a href="#">Santoferrara, Luciana</a>	Hofstra University	Co-Principal Investigator
<a href="#">Soenen, Karen</a>	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

## Abstract

Seven stations on the shelf and slope south of Montauk, NY on 14-15 June 2022 were sampled. Basic hydrographic properties, including temperature, salinity, dissolved oxygen, and pH were measured and rosette samples were taken for chlorophyll, nutrients, and microplankton. Water was filtered for metagenomics and metatranscriptomics and picked individual microplankters for sequencing. Three to ten depths were sampled at each station. Our shallowest station was on the shelf at 38m and the deepest was at the slope edge at 2400m. Due to limitations of the CTD our deepest sampled depth was 1150m. At the two shallowest stations, we also deployed a Wetstar fluorometer for phytoplankton fluorescence. The CTD data were processed with SeaBird's Seasoft program and converted to spreadsheet format.

## Table of Contents

- [Coverage](#)
- [Dataset Description](#)
  - [Acquisition Description](#)
  - [Processing Description](#)
- [Data Files](#)
- [Parameters](#)
- [Instruments](#)
- [Project Information](#)
- [Funding](#)

## Coverage

**Spatial Extent:** N:40.994 E:-71.3587 S:39.3804 W:-71.7138

**Temporal Extent:** 2022-06-14 - 2022-06-15

## Acquisition Description

Seven stations on the shelf and slope south of Montauk, NY on 14-15 June 2022 were sampled. Basic hydrographic properties, including temperature, salinity, dissolved oxygen, and pH were measured and rosette samples were taken for chlorophyll, nutrients, and microplankton. Water was filtered for metagenomics and metatranscriptomics and picked individual microplankters for sequencing. Three to ten depths were sampled at each station. Our shallowest station was on the shelf at 38m and the deepest was at the slope edge at 2400m. Due to limitations of the CTD our deepest sampled depth was 1150m. At the two shallowest stations,

we also deployed a Wetstar fluorometer for phytoplankton fluorescence.

## Processing Description

The CTD data were processed with SeaBird's Seasoft program and converted to spreadsheet format.

[ [table of contents](#) | [back to top](#) ]

---

## Data Files

File	Version
<b>CTD_files</b> filename: CTD_files.zip <small>(ZIP Archive (ZIP), 2.94 MB) MD5:5587a53921ab10da5f12fdad02145331</small> <i>Original CTD Seabird files for RV Connecticut Cruise June 2022. Files are divided up per station number.</i>	1

[ [table of contents](#) | [back to top](#) ]

---

## Parameters

Parameter	Description	Units
Station	Station number	unitless
latitude	Station latitude, south is negative	decimal degrees
longitude	Station longitude, west is negative	decimal degrees
Date	Date of CTD sampling	unitless
Time	Start time of CTD sampling	unitless
density	Density	kg/m <sup>3</sup>
depth	Depth	meters (m)
Fluorescence	Fluorescence, arbitrary	mg/m <sup>3</sup>
oxygen	dissolved oxygen	mg/L
pH	pH	unitless
salinity	Salinity	unitless
scan	sampling event number for station	unitless
Temperature	Temperature	Degrees Celsius (°C)
flag	Quality flag	unitless
ISO_DateTime_Local	Sampling date and time (Eastern Daylight Time (GMT-4)) in ISO 8601 format yyyy-mm-ddTHH:MM:SS	units
ISO_DateTime_UTC	Sampling date and time (UTC) in ISO 8601 format yyyy-mm-ddTHH:MM:SSZ	units

[ [table of contents](#) | [back to top](#) ]

---

## Instruments

<b>Dataset-specific Instrument Name</b>	
<b>Generic Instrument Name</b>	CTD Sea-Bird 9
<b>Generic Instrument Description</b>	The Sea-Bird SBE 9 is a type of CTD instrument package. The SBE 9 is the Underwater Unit and is most often combined with the SBE 11 Deck Unit (for real-time readout using conductive wire) when deployed from a research vessel. The combination of the SBE 9 and SBE 11 is called a SBE 911. The SBE 9 uses Sea-Bird's standard modular temperature and conductivity sensors (SBE 3 and SBE 4). The SBE 9 CTD can be configured with auxiliary sensors to measure other parameters including dissolved oxygen, pH, turbidity, fluorometer, altimeter, etc.). Note that in most cases, it is more accurate to specify SBE 911 than SBE 9 since it is likely a SBE 11 deck unit was used. more information from Sea-Bird Electronics

<b>Dataset-specific Instrument Name</b>	Wetstar fluorometer
<b>Generic Instrument Name</b>	WETLabs WETStar fluorometer
<b>Dataset-specific Description</b>	Wetstar fluorometer for phytoplankton fluorescence
<b>Generic Instrument Description</b>	Submersible fluorometer designed for through-flow or pumped CTD applications manufactured by WetLabs and which can be configured for various types of fluorescence. The probe has a temperature range of 0-30 degrees C and a depth rating of 600m.

[ [table of contents](#) | [back to top](#) ]

## Project Information

**Collaborative Research: Combining single-cell and community 'omics' to test hypotheses about diversity and function of planktonic ciliates (Ciliate Omics)**

**Website:** <http://microzooplankton.uconn.edu>

**Coverage:** New England continental shelf

### *NSF Award Abstract:*

Planktonic ciliates are key members of marine food webs where they serve diverse roles, including as food chain links between smaller microbes and larger plankton. Due to their small size and difficulties in identifying and cultivating them, we know less about ciliate diversity and distributions in the ocean than we do about larger organisms such as fish and invertebrates. Previous work from this team measured ciliate diversity in coastal waters and found that distinct genetic variants were separated in time and space in a way that could be related to factors such as ocean temperature, salinity, and depth gradients. Many questions remained unanswered, and it is important to understand the environmental factors that control the diversity and distribution of plankton such as ciliates to predict how these organisms may respond to a changing environment in the coming decades. This project focuses on: 1) how ciliate species are delineated using single-cell genomics and transcriptomics; 2) DNA-based studies of all ciliates and other planktonic members of the SAR clade (Stramenopila, Alveolata, Rhizaria), which will provide ecological context; 3) in situ gene expression by single-cell and meta-transcriptomics; and 4) laboratory studies of gene expression in cultivated ciliate species. This project involves training of postdoctoral scholars, graduate students, and undergraduates. The researchers are committed to creating diverse and inclusive research labs; recruitment of participants will be done through

partnership with appropriate groups on our campuses. The project integrates with summer Research Experiences for Undergraduates (REU) activities at both Smith College and UCONN (including the UCONN/Mystic Aquarium joint REU), which are especially focused on underrepresented students. This project also enhances efforts to broaden understanding of biodiversity in partnership with the UCONN Noyce Scholars Program, which facilitates career-changing STEM professionals to become teachers in underserved secondary schools.

This project will assess distributions of reproductively-isolated species, determined using a new method to characterize regions of the ciliate germline genome. Furthermore, it will use phylogenomic methods to identify clade-specific transcripts (e.g. those of spirotrich ciliates) within metatranscriptomes from the shelf environment and to expand knowledge of ciliate function with single-cell transcriptomics of field-collected cells. These approaches will be a substantial improvement over the culture-based methods that are potentially biased towards "weedy" species in the ocean. The combination of definitive species identification with assessment of function via single-cell and meta- transcriptomics promises to provide significant advances in marine plankton ecology. The research focuses on two broad questions: 1) does the observed high diversity in phylogenetically-informative genes reflect reproductive isolation and functional differentiation in planktonic ciliates? and 2) do different co-occurring species of planktonic ciliates show substantial functional differences that correspond to different niches in the ocean? The project assesses species boundaries (i.e. reproductive isolation) through analyses of patterns in the germline micronuclei of planktonic ciliate morphospecies; characterizes transitions of closely-related ciliates across ecological gradients in the ocean; and examines functional differences within and between species, and in communities, through analyses of transcriptomics.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

[ [table of contents](#) | [back to top](#) ]

---

## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1924570</a>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1924527</a>

[ [table of contents](#) | [back to top](#) ]